

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/511, 455
Source: PCT
Date Processed by STIC: 11/28/2005

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PCT

RAW SEQUENCE LISTING

DATE: 11/28/2005

PATENT APPLICATION: US/10/511,455

TIME: 15:39:25

Input Set : A:\9013.63 Sequence Listing CRF.TXT

Output Set: N:\CRF4\11282005\J511455.raw

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3 <110> APPLICANT: Pickard, Benjamin Simon
4     Blackwood, Douglas
5     Porteous, David
6     Muir, Walter John
7     Mors, Ole
8     Ewald, Henrik Lykke
10 <120> TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES
12 <130> FILE REFERENCE: 9013.63
14 <140> CURRENT APPLICATION NUMBER: US 10/511,455
15 <141> CURRENT FILING DATE: 2004-10-05
17 <150> PRIOR APPLICATION NUMBER: PCT/GB03/001543
18 <151> PRIOR FILING DATE: 2003-04-07
20 <150> PRIOR APPLICATION NUMBER: GB0207902.8
21 <151> PRIOR FILING DATE: 2002-04-05
23 <150> PRIOR APPLICATION NUMBER: GB0207904.4
24 <151> PRIOR FILING DATE: 2002-04-05
26 <150> PRIOR APPLICATION NUMBER: GB0207900.2
27 <151> PRIOR FILING DATE: 2002-04-05
29 <150> PRIOR APPLICATION NUMBER: GB0207901.0
30 <151> PRIOR FILING DATE: 2002-04-05
32 <150> PRIOR APPLICATION NUMBER: GB0227734.1
33 <151> PRIOR FILING DATE: 2002-11-28
35 <160> NUMBER OF SEQ ID NOS: 94
37 <170> SOFTWARE: PatentIn version 3.1
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40 <211> LENGTH: 4773
41 <212> TYPE: DNA
42 <213> ORGANISM: Homo sapiens
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49 ccctggaatg aaataaataa ataaagaccg taagtgtgta gatagcgggc cccaagatat      180
51 ttttagtcct ctgcaatcag ccactagagg aagggggagg gagaagggag taaaaaagtt      240
53 ttgatccgtt cgggaagggg ctgcaagaga acccttggga gaaagcagta gcctcagctc      300
55 caaactcagc gagcttttct cggctggcgt tttgtctcct atagcgtaga ctgtaagaga      360
57 acagaaagga gtttcccgag aagattcagg ctggcgctcct gggctggccc gtcccttctg      420
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61 ctggcgggag gcatccaagg cacgatgtat gtgcgctcgc gctcgcgcaa atacggccgg      540
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77	gcgacgcgcg	gctgcggccg	ggtggtcaag	ctgcagcagc	tgccggagca	cctcgagcgc	1020
79	tgcgacttcg	cgcccgcgcg	ctgtccgccac	gcgggttgcg	gccagggtgt	gctgcggcgc	1080
81	gacgtggagg	cgcacatgcg	cgacgcgtgc	gacgcgcggc	cagtggggccg	ctgccaggag	1140
83	ggctgcgggc	tacccttgac	gcacggcgag	cagcgcgcgg	gcggccactg	ctgcgcgcga	1200
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87	aagaaggagg	cgctgcgcgc	tgggaagcgc	gagaagtgcg	tgggtggccca	gctggccgcg	1320
89	gcgcagcttg	agctgcagat	gaccgcgctg	cgctaccaga	agaaattcac	cgaatacagc	1380
91	gcgcgcctcg	actcgcctcag	ccgctgcgtg	gccgcgccgc	ccggcggcaa	gggcgaagaa	1440
93	acaaaaagtc	tgactcttgt	cctgcacgcg	gactccggct	ccctgggatt	caatattatt	1500
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107	ctcttgccag	aggagcatcc	ctcagcccat	gaatactacg	atccaaatga	ctacattgga	1920
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139	gccacaaga	tgagcagct	caaggagcag	taccgcgagt	cctggatgct	gcacaacagc	2880
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149	tccaagaatc	tgctctccat	cacggaagat	cccgaagtgg	gcacccctac	ctatagcccc	3180
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161	atccgcagcg	acgggacgcg	ctacatcacc	aagaggcccg	tgccgggacc	cctgctgcgg	3540
163	gagcgcgccc	tgaagatccg	ggaagagcgc	agcggcatga	ccaccgacga	cgacgcgggt	3600
165	agcgagatga	agatggggcg	ctactggagc	aaggaggaga	ggaagcagca	cctgggtgaag	3660
167	gccaaggagc	agcggcggcg	gcgcgagttc	atgatgcaga	gcaggttgga	ttgtctcaag	3720
169	gagcagcaag	cagccgatga	caggaaggag	atgaacattc	tcgaactgag	ccacaaaaag	3780

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177 aattcctgcc tcgttcaatg cggcaagttt ttgtatataa gataagtacg gtcttcatgt 4020
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199 gttgtggatg gagacggttt gtggaatttt aagtgtcat tgtagtaaac ttttgctttg 4680
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206 <210> SEQ ID NO: 2

207 <211> LENGTH: 1066

208 <212> TYPE: PRT

209 <213> ORGANISM: Homo sapiens

211 <400> SEQUENCE: 2

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218 20 25 30
221 Cys Gly His Val Phe Cys Ala Gly Cys Val Leu Pro Trp Val Val Gln
222 35 40 45
225 Glu Gly Ser Cys Pro Ala Arg Cys Arg Gly Arg Leu Ser Ala Lys Glu
226 50 55 60
229 Leu Asn His Val Leu Pro Leu Lys Arg Leu Ile Leu Lys Leu Asp Ile
230 65 70 75 80
233 Lys Cys Ala Tyr Ala Thr Arg Gly Cys Gly Arg Val Val Lys Leu Gln
234 85 90 95
237 Gln Leu Pro Glu His Leu Glu Arg Cys Asp Phe Ala Pro Ala Arg Cys
238 100 105 110
241 Arg His Ala Gly Cys Gly Gln Val Leu Leu Arg Arg Asp Val Glu Ala
242 115 120 125
245 His Met Arg Asp Ala Cys Asp Ala Arg Pro Val Gly Arg Cys Gln Glu
246 130 135 140
249 Gly Cys Gly Leu Pro Leu Thr His Gly Glu Gln Arg Ala Gly Gly His
250 145 150 155 160
253 Cys Cys Ala Arg Ala Leu Arg Ala His Asn Gly Ala Leu Gln Ala Arg
254 165 170 175
257 Leu Gly Ala Leu His Lys Ala Leu Lys Lys Glu Ala Leu Arg Ala Gly
258 180 185 190
261 Lys Arg Glu Lys Ser Leu Val Ala Gln Leu Ala Ala Ala Gln Leu Glu
262 195 200 205
265 Leu Gln Met Thr Ala Leu Arg Tyr Gln Lys Lys Phe Thr Glu Tyr Ser

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273	Lys	Gly	Glu	Glu	Thr	Lys	Ser	Leu	Thr	Leu	Val	Leu	His	Arg	Asp	Ser	
274					245					250					255		
277	Gly	Ser	Leu	Gly	Phe	Asn	Ile	Ile	Gly	Gly	Arg	Pro	Ser	Val	Asp	Asn	
278				260					265					270			
281	His	Asp	Gly	Ser	Ser	Ser	Glu	Gly	Ile	Phe	Val	Ser	Lys	Ile	Val	Asp	
282			275						280				285				
285	Ser	Gly	Pro	Ala	Ala	Lys	Glu	Gly	Gly	Leu	Gln	Ile	His	Asp	Arg	Ile	
286		290					295				300						
289	Ile	Glu	Val	Asn	Gly	Arg	Asp	Leu	Ser	Arg	Ala	Thr	His	Asp	Gln	Ala	
290	305					310					315					320	
293	Val	Glu	Ala	Phe	Lys	Thr	Ala	Lys	Glu	Pro	Ile	Val	Val	Gln	Val	Leu	
294					325					330					335		
297	Arg	Arg	Thr	Pro	Arg	Thr	Lys	Met	Phe	Thr	Pro	Pro	Ser	Glu	Ser	Gln	
298				340					345					350			
301	Leu	Val	Asp	Thr	Gly	Thr	Gln	Thr	Asp	Ile	Thr	Phe	Glu	His	Ile	Met	
302			355					360					365				
305	Ala	Leu	Thr	Lys	Met	Ser	Ser	Pro	Ser	Pro	Pro	Val	Leu	Asp	Pro	Tyr	
306		370					375				380						
309	Leu	Leu	Pro	Glu	Glu	His	Pro	Ser	Ala	His	Glu	Tyr	Tyr	Asp	Pro	Asn	
310	385					390					395					400	
313	Asp	Tyr	Ile	Gly	Asp	Ile	His	Gln	Glu	Met	Asp	Arg	Glu	Glu	Leu	Glu	
314				405					410						415		
317	Leu	Glu	Glu	Val	Asp	Leu	Tyr	Arg	Met	Asn	Ser	Gln	Asp	Lys	Leu	Gly	
318				420					425					430			
321	Leu	Thr	Val	Cys	Tyr	Arg	Thr	Asp	Asp	Glu	Asp	Asp	Ile	Gly	Ile	Tyr	
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329	Arg	Glu	Gly	Asp	Arg	Ile	Ile	Gln	Ile	Asn	Gly	Ile	Glu	Val	Gln	Asn	
330	465					470				475						480	
333	Arg	Glu	Glu	Ala	Val	Ala	Leu	Leu	Thr	Ser	Glu	Glu	Asn	Lys	Asn	Phe	
334				485					490					495			
337	Ser	Leu	Leu	Ile	Ala	Arg	Pro	Glu	Leu	Gln	Leu	Asp	Glu	Gly	Trp	Met	
338			500					505						510			
341	Asp	Asp	Asp	Arg	Asn	Asp	Phe	Leu	Asp	Asp	Leu	His	Met	Asp	Met	Leu	
342			515				520					525					
345	Glu	Glu	Gln	His	His	Gln	Ala	Met	Gln	Phe	Thr	Ala	Ser	Val	Leu	Gln	
346		530					535					540					
349	Gln	Lys	Lys	His	Asp	Glu	Asp	Gly	Gly	Thr	Thr	Asp	Thr	Ala	Thr	Ile	
350	545					550					555					560	
353	Leu	Ser	Asn	Gln	His	Glu	Lys	Asp	Ser	Gly	Val	Gly	Arg	Thr	Asp	Glu	
354				565					570					575			
357	Ser	Thr	Arg	Asn	Asp	Glu	Ser	Ser	Glu	Gln	Glu	Asn	Asn	Gly	Asp	Asp	
358			580						585					590			
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370 625                      630                      635                      640
373 Asp Glu Cys Glu Arg Phe Arg Glu Leu Leu Glu Leu Lys Cys Gln Val
374      645                      650                      655
377 Lys Ser Ala Thr Pro Tyr Gly Leu Tyr Tyr Pro Ser Gly Pro Leu Asp
378      660                      665                      670
381 Ala Gly Lys Ser Asp Pro Glu Ser Val Asp Lys Glu Leu Glu Leu Leu
382      675                      680                      685
385 Asn Glu Glu Leu Arg Ser Ile Glu Leu Glu Cys Leu Ser Ile Val Arg
386      690                      695                      700
389 Ala His Lys Met Gln Gln Leu Lys Glu Gln Tyr Arg Glu Ser Trp Met
390 705                      710                      715                      720
393 Leu His Asn Ser Gly Phe Arg Asn Tyr Asn Thr Ser Ile Asp Val Arg
394      725                      730                      735
397 Arg His Glu Leu Ser Asp Ile Thr Glu Leu Pro Glu Lys Ser Asp Lys
398      740                      745                      750
401 Asp Ser Ser Ser Ala Tyr Asn Thr Gly Glu Ser Cys Arg Ser Thr Pro
402      755                      760                      765
405 Leu Thr Leu Glu Ile Ser Pro Asp Asn Ser Leu Arg Arg Ala Ala Glu
406      770                      775                      780
409 Gly Ile Ser Cys Pro Ser Ser Glu Gly Ala Val Gly Thr Thr Glu Ala
410 785                      790                      795                      800
413 Tyr Gly Pro Ala Ser Lys Asn Leu Leu Ser Ile Thr Glu Asp Pro Glu
414      805                      810                      815
417 Val Gly Thr Pro Thr Tyr Ser Pro Ser Leu Lys Glu Leu Asp Pro Asn
418      820                      825                      830
421 Gln Pro Leu Glu Ser Lys Glu Arg Arg Ala Ser Asp Gly Ser Arg Ser
422      835                      840                      845
425 Pro Thr Pro Ser Gln Lys Leu Gly Ser Ala Tyr Leu Pro Ser Tyr His
426      850                      855                      860
429 His Ser Pro Tyr Lys His Ala His Ile Pro Ala His Ala Gln His Tyr
430 865                      870                      875                      880
433 Gln Ser Tyr Met Gln Leu Ile Gln Gln Lys Ser Ala Val Glu Tyr Ala
434      885                      890                      895
437 Gln Ser Gln Met Ser Leu Val Ser Met Cys Lys Asp Leu Ser Ser Pro
438      900                      905                      910
441 Thr Pro Ser Glu Pro Arg Met Glu Trp Lys Val Lys Ile Arg Ser Asp
442      915                      920                      925
445 Gly Thr Arg Tyr Ile Thr Lys Arg Pro Val Arg Asp Arg Leu Leu Arg
446      930                      935                      940
449 Glu Arg Ala Leu Lys Ile Arg Glu Glu Arg Ser Gly Met Thr Thr Asp
450 945                      950                      955                      960
453 Asp Asp Ala Val Ser Glu Met Lys Met Gly Arg Tyr Trp Ser Lys Glu
454      965                      970                      975
457 Glu Arg Lys Gln His Leu Val Lys Ala Lys Glu Gln Arg Arg Arg Arg
458      980                      985                      990
461 Glu Phe Met Met Gln Ser Arg Leu Asp Cys Leu Lys Glu Gln Gln Ala

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220>

to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:94; N Pos. 4,5

VERIFICATION SUMMARY

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L:5592 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:94 after pos.:0